

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Maertens, Geert  
Bosman, Fons  
De Martynoff, Guy  
Buyse, Marie-Ange
- (ii) TITLE OF INVENTION: Purified hepatitis C virus envelope  
proteins for diagnostic and therapeutic use.
- (iii) NUMBER OF SEQUENCES: 122
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: NIXON & VANDERHVE
  - (B) STREET: 1100 North Glebe Road, 8th Floor
  - (C) CITY: Arlington, VA 22201
  - (E) COUNTRY: USA
  - (F) ZIP: 22201
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unassigned
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sadoff, B. J.
  - (B) REGISTRATION NUMBER: 36663
  - (C) REFERENCE/DOCKET NUMBER: 2551-61
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 816-4000
  - (B) TELEFAX: (703) 816-4100

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCATGCAAG CTTAATTAAT T

21

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CCGGGGAGGC CTGCACGTGA TCGAGGGCAG ACACCATCAC CACCATCACT AATAGTTAAT

60

TAACTGCA

68

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 642 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..639

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA CTG TCC TGT  
 Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys  
 1 5 10 15

48

CTG ACC ATT CCA GCT TCC GCT TAT GAG GTG CGC AAC GTG TCC GGG ATG  
 Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Met  
 20 25 30

96

TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA  
 Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala

144

35	40	45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG			192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu			
50	55	60	
AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG CTC GCA GCT			240
Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala			
65	70	75	80
AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC GTC GAT TTG			288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu			
	85	90	95
CTC GTT GGG GCG GCT GCT CTC TGT TCC GCT ATG TAC GTG GGG GAT CTC			336
Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met Tyr Val Gly Asp Leu			
	100	105	110
TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC TCG CCT CGC			384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg			
	115	120	125
CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC			432
Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
	130	135	140
ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT			480
Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro			
	145	150	155
ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC			528
Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val			
	165	170	175
GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC			576
Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala			
	180	185	190
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA			624
Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu			
	195	200	205
CTC TTT GCT CTC TAATAG			642
Leu Phe Ala Leu			
210			

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1						5				10				15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met

20										25					30															
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala															
		35						40					45																	
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu															
	50					55				60																				
Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala															
	65				70					75					80															
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu															
				85					90					95																
Leu	Val	Gly	Ala	Ala	Ala	Leu	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu															
		100						105					110																	
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg															
		115					120					125																		
Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His															
		130				135						140																		
Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro															
	145				150				155					160																
Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val															
			165					170						175																
Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala															
		180					185						190																	
Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile	Val	Met	Leu															
		195					200					205																		
Leu	Phe	Ala	Leu																											
		210																												

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..792

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..789

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	
CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGT CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT	768

Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Ile  
 245 250 255

GTG ATG CTA CTC TTT GCT CCC TAATAG  
 Val Met Leu Leu Phe Ala Pro  
 260

795

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu  
 1 5 10 15

Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg  
 20 25 30

Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala  
 35 40 45

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu  
 50 55 60

Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val  
 65 70 75 80

Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val  
 85 90 95

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
 100 105 110

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205

Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro  
 210 215 220

Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala

225		230		235		240									
Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Ile
				245					250					255	
Val	Met	Leu	Leu	Phe	Ala	Pro									
				260											

## (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..630

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..627

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC	GCC	GAC	CTC	48
Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	
1				5					10					15		
ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	CTA	GGG	GGT	GCT	GCC	AGA	96
Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	
			20					25					30			
GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	144
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	
			35				40					45				
ACA	GGG	AAT	TTG	CCT	GGT	TGC	TCT	TTC	TCT	ATC	FTC	CTC	TTG	GCT	TTA	192
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	
	50					55					60					
CTG	TCC	TGT	CTG	ACC	ATT	CCA	GCT	TCC	GCT	TAT	GAG	GTG	CGC	AAC	GTG	240
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	
	65				70					75					80	
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	
				85					90					95		
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	
			100					105					110			

GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACT ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACA GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TAATAG	633
Trp	
210	

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	



Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val  
 145 150 155 160

Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile  
 165 170 175

Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr  
 180 185 190

Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn  
 195 200 205

Trp

(2) INFORMATION FOR SEQ ID NO: 9:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 483 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..480

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	

GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT	432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	
130 135 140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TCC TAATAG	483
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser	
145 150 155 160	

## (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	
115 120 125	
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His	

130 135 140  
 Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..477

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..474

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG TCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCC CTG CTG TCC TGT	48
Met Ser Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys	
1 5 10 15	
CTG ACC ATA CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG TCC GGG GTG	96
Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val Ser Gly Val	
20 25 30	
TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATA GTG TAT GAG GCA	144
Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala	
35 40 45	
GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT CGG GAG	192
Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val Arg Glu	
50 55 60	
GGC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT CCC ACG CTC GCG GCC	240
Gly Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala	
65 70 75 80	
AGG AAC GCC AGC GTC CCC ACA ACG ACA ATA CGA CGC CAC GTC GAT TTG	288
Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu	
85 90 95	
CTC GTT GGG GCT GCT GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC	336
Leu Val Gly Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu	
100 105 110	
TGC GGA TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCA CCT CGC	384
Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg	

115	120	125	
CGG CAT CAA ACA GTA CAG GAC TGC AAC TGC TCA ATC TAT CCC GGC CAT			432
Arg His Gln Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His			
130	135	140	
GTA TCA GGT CAC CGC ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG			480
Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp			
145	150	155	

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ser	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys
1				5					10					15	
Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val
			20					25					30		
Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala
		35				40						45			
Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu
	50					55				60					
Gly	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala
65					70					75					80
Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu
			85						90					95	
Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu
			100					105					110		
Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
	115						120					125			
Arg	His	Gln	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His
130						135					140				
Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp		
145					150					155					

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..633

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATG CTG GGT AAG GCC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Ala Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAA GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTA	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTA ACC ATT CCA GCT TCC GCT TAC GAG GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCG GCT AGG AAC GCC AGC ATC CCC ACT ACA ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Ile Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAT CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	

180	185	190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC			624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn			
195	200	205	
TGG TAC TAATAG			
Trp Tyr			640
210			

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Leu	Gly	Lys	Ala	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
			35				40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70					75					80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
			115				120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
			130				135					140			
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
	145				150				155					160	
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
				165				170					175		
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
			195				200					205			

Trp Tyr  
210

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATGCCCCGGTT GCTCTTTCTC TATCTT

26

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGTTGGGTA AGGTCATCGA TACCCT

26

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CTATTAGGAC CAGTTCATCA TCATATCCCA

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTATTACCAG TTCATCATCA TATCCCA

27

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATACGACGCC ACGTCGATTC CCAGCTGTTT ACCATC

36

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GATGGTGAAC AGCTGGGAAT CGACGTGGCG TCGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..720

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	

145		150		155		160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT							528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg							
	165			170		175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG							576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val							
	180			185		190	
GTA TCG CAG CTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG							624
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala							
	195			200		205	
GGG GCC CAT TGG GGA GTC CTG GCG GGT CTC GCC TAC TAT TCC ATG GTG							672
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val							
	210			215		220	
GGG AAC TGG GCT AAG GTT TTG ATT GTG ATG CTA CTC TTT GCT CCC TAATAG							723
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro							
	225			230		235	240

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35				40						45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55				60					
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65				70					75				80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
		100						105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
		115					120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
	130					135						140			
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val

145		150		155		160
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg						
		165		170		175
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val						
		180		185		190
Val Ser Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala						
		195		200		205
Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val						
		210		215		220
Gly Asn Trp Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Pro						
225		230		235		

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..558

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..555

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	

65	70	75	80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG				288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	85	90	95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC				336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	100	105	110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG				384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	115	120	125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC				432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	130	135	140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG				480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	145	150	155	160
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT				528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	165	170	175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TAATAG				561
Met Ala Trp Asp Met Met Met Asn Trp	180	185		

## (2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5				10						15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala
		35					40					45			
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
		50				55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
		65			70				75					80	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
 115 120 125

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
 130 135 140

Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val  
 145 150 155 160

Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg  
 165 170 175

Met Ala Trp Asp Met Met Met Asn Trp  
 180 185

## (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..603

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..600

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT TCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	

TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TCC CAG CTG TTC ACC ATC TCG CCT CGC CGG CAT GAG ACG GTG	480
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val	
145 150 155 160	
CAG GAC TGC AAT TGC TCA ATC TAT CCC GGC CAC ATA ACG GGT CAC CGT	528
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg	
165 170 175	
ATG GCT TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG	576
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val	
180 185 190	
GTA TCG CAG CTG CTC CGG ATC CTC TAATAG	606
Val Ser Gln Leu Leu Arg Ile Leu	
195 200	

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	

Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys  
                   100                  105                  110  
 Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr  
                   115                  120                  125  
 Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His  
                   130                  135                  140  
 Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val  
                   145                  150                  155                  160  
 Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg  
                   165                  170                  175  
 Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val  
                   180                  185                  190  
 Val Ser Gln Leu Leu Arg Ile Leu  
                   195                  200

## (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 636 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..630

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATG TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Met Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1                  5                  10                  15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20                  25                  30	
GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35                  40                  45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192

Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu		
50						55					60						
CTG	TCC	TGT	CTG	ACC	GTT	CCA	GCT	TCC	GCT	TAT	GAA	GTG	CGC	AAC	GTG	240	
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val	80	
65					70					75							
TCC	GGG	ATG	TAC	CAT	GTC	ACG	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	288	
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	95	
				85					90								
TAT	GAG	GCA	GCG	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	336	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	110	
			100					105									
GTT	CGG	GAG	AAC	AAC	TCT	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACC	CCC	ACG	384	
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	125	
		115					120										
CTC	GCA	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	ACA	ATA	CGA	CGC	CAC	432	
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Ile	Arg	Arg	His			
			130				135					140					
GTC	GAT	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCT	CGC	CGG	CAT	GAG	ACG	GTG	480	
Val	Asp	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	160	
				150						155							
CAG	GAC	TGC	AAT	TGC	TCA	ATC	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	CGT	528	
Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	175	
				165					170								
ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACG	GCC	CTG	GTG	576	
Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	190	
			180					185									
GTA	TCG	CAG	CTG	CTC	CGG	ATC	GTG	ATC	GAG	GGC	AGA	CAC	CAT	CAC	CAC	624	
Val	Ser	Gln	Leu	Leu	Arg	Ile	Val	Ile	Glu	Gly	Arg	His	His	His	His	205	
			195				200										
CAT	CAC	TAATAG														636	
His	His															210	

## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu
1				5					10					15	
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg
			20					25					30		
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala



35	40	45
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu		
50	55	60
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val		
65	70	75
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val		
	85	90
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys		
	100	105
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr		
	115	120
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His		
	130	135
Val Asp Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val		
145	150	155
Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg		
	165	170
Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val		
	180	185
Val Ser Gln Leu Leu Arg Ile Val Ile Glu Gly Arg His His His His		
	195	200
His His		205
210		

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..627

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..624

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGA TTC GCC GAT CTC ATG

Met	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	
1				5					10					15		
GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	GTA	GGA	GGC	GTC	GCA	AGA	GCC	96
Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	
			20					25					30			
CTT	GCG	CAT	GGC	GTG	AGG	GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	144
Leu	Ala	His	Gly	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	
		35					40					45				
GGG	AAT	TTG	CCC	GGT	TGC	TCC	TTT	TCT	ATT	TTC	CTT	CTC	GCT	CTG	TTC	192
Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe	
	50					55					60					
TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT	CTA	GAG	TGG	CGG	AAT	ACG	TCT	240
Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser	Leu	Glu	Trp	Arg	Asn	Thr	Ser	
	65				70					75					80	
GGC	CTC	TAT	GTC	CTT	ACC	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAC	288
Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	
				85					90					95		
GAG	GCC	GAT	GAC	GTT	ATT	CTG	CAC	ACA	CCC	GGC	TGC	ATA	CCT	TGT	GTC	336
Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr	Pro	Gly	Cys	Ile	Pro	Cys	Val	
			100					105					110			
CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	CCT	ACA	GTG	384
Gln	Asp	Gly	Asn	Thr	Ser	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	
		115					120					125				
GCA	GTC	AAG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	TCG	ATA	CGC	AGT	CAT	GTG	432
Ala	Val	Lys	Tyr	Val	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	
	130					135					140					
GAC	CTA	TTA	GTG	GGC	GCG	GCC	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	480
Asp	Leu	Leu	Val	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	
	145			150					155					160		
GAC	ATG	TGT	GGG	GCT	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	528
Asp	Met	Cys	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	
			165					170						175		
CCT	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	TAC	CCA	576
Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	
			180				185						190			
GGC	CAT	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	ATG	ATG	ATG	AAC	TGG	624
Gly	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
		195					200					205				
TAATAG																634

## (2) INFORMATION FOR SEQ ID NO: 30:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1           5           10           15

Gly Tyr Ile Pro Leu Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala
          20           25           30

Leu Ala His Gly Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr
          35           40           45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
          50           55           60

Ser Cys Leu Ile His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser
          65           70           75           80

Gly Leu Tyr Val Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr
          85           90           95

Glu Ala Asp Asp Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val
          100           105           110

Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val
          115           120           125

Ala Val Lys Tyr Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val
          130           135           140

Asp Leu Leu Val Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly
          145           150           155           160

Asp Met Cys Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg
          165           170           175

Pro Arg Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro
          180           185           190

Gly His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
          195           200           205

```

## (2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..627

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..624

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC GCC GAT CTC ATG	48
Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met	
1 5 10 15	
GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT GGG GGC GTC GCA AGG GCT	96
Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala	
20 25 30	
CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA	144
Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr	
35 40 45	
GGG AAT TTA CCC GGT TGC TCT TTC TCT ATC TTT ATT CTT GCT CTT CTC	192
Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu	
50 55 60	
TCG TGT CTG ACC GTT CCG GCC TCT GCA GTT CCC TAC CGA AAT GCC TCT	240
Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser	
65 70 75 80	
GGG ATT TAT CAT GTT ACC AAT GAT TGC CCA AAC TCT TCC ATA GTC TAT	288
Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr	
85 90 95	
GAG GCA GAT AAC CTG ATC CTA CAC GCA CCT GGT TGC GTG CCT TGT GTC	336
Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val	
100 105 110	
ATG ACA GGT AAT GTG AGT AGA TGC TGG GTC CAA ATT ACC CCT ACA CTG	384
Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu	
115 120 125	
TCA GCC CCG AGC CTC GGA GCA GTC ACG GCT CCT CTT CGG AGA GCC GTT	432
Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val	
130 135 140	
GAC TAC CTA GCG GGA GGG GCT GCC CTC TGC TCC GCG TTA TAC GTA GGA	480
Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly	
145 150 155 160	
GAC GCG TGT GGG GCA CTA TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG	528
Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg	
165 170 175	
CCT CGC CAG CAC GCT ACG GTG CAG AAC TGC AAC TGT TCC ATT TAC AGT	576
Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser	
180 185 190	
GGC CAT GTT ACC GGC CAC CGG ATG GCA TGG GAT ATG ATG ATG AAC TGG	624
Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp	
195 200 205	

TAATAG

630

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

Met Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu Met
 1             5             10             15

Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile Gly Gly Val Ala Arg Ala
          20             25             30

Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr
          35             40             45

Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
          50             55             60

Ser Cys Leu Thr Val Pro Ala Ser Ala Val Pro Tyr Arg Asn Ala Ser
          65             70             75             80

Gly Ile Tyr His Val Thr Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr
          85             90             95

Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val
          100            105            110

Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile Thr Pro Thr Leu
          115            120            125

Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val
          130            135            140

Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly
          145            150            155            160

Asp Ala Cys Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg
          165            170            175

Pro Arg Gln His Ala Thr Val Gln Asn Cys Asn Cys Ser Ile Tyr Ser
          180            185            190

Gly His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
          195            200            205

```

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
 TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
 CTATTATGGT GGTAAGCCAC AGAGCAGGAG

30

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1473

(ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..1470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
 TGG GAT ATG ATG ATG AAC TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG

48

Trp	Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser		
1					5				10						15		
CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	GTG	GCG	GGG	GCC		96
Gln	Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala		
			20					25					30				
CAT	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	TAC	TAT	TCC	ATG	GTG	GGG	AAC		144
His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn		
		35					40					45					
TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	GCC	GCG	GTC	GAC	GGG		192
Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly		
	50						55				60						
CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	GAT	ACC	AGG	GGC	CTT		240
His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu		
	65				70					75					80		
GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC		288
Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn		
				85					90					95			
ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC		336
Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp		
			100					105					110				
TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC		384
Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe		
		115					120					125					
AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC		432
Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp		
	130					135					140						
AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC		480
Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser		
	145				150					155					160		
TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT		528
Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly		
				165					170					175			
ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG		576
Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro		
			180					185					190				
AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT		624
Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr		
		195					200					205					
AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG		672
Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg		
	210					215					220						
CCG	CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG		720
Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly		
	225				230					235					240		
TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC		768
Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly		
				245					250					255			

AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu 260 265 270	816
GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys 275 280 285	864
ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn 290 295 300	912
TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg 305 310 315 320	960
TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu 325 330 335	1008
GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GAG Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu 340 345 350	1056
TGG CAG ATA CTG CCC TGT TCC TTC ACC ACC CTG CCG GCC CTA TCC ACC Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr 355 360 365	1104
GGC CTG ATC CAC CTC CAT CAG AAC ATC GTG GAC GTG CAA TAC CTG TAC Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr 370 375 380	1152
GGT GTA GGG TCG GCG GTT GTC TCC CTT GTC ATC AAA TGG GAG TAT GTC Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val 385 390 395 400	1200
CTG TTG CTC TTC CTT CTC CTG GCA GAC GCG CGC ATC TGC GCC TGC TTA Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu 405 410 415	1248
TGG ATG ATG CTG CTG ATA GCT CAA GCT GAG GCC GCC TTA GAG AAC CTG Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu 420 425 430	1296
GTG GTC CTC AAT GCG GCG GCC GTG GCC GGG GCG CAT GGC ACT CTT TCC Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser 435 440 445	1344
TTC CTT GTG TTC TTC TGT GCT GCC TGG TAC ATC AAG GGC AGG CTG GTC Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460	1392
CCT GGT GCG GCA TAC GCC TTC TAT GGC GTG TGG CCG CTG CTC CTG CTT Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 465 470 475 480	1440
CTG CTG GCC TTA CCA CCA CGA GCT TAT GCC TAGTAA Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 485 490	1476



## (2) INFORMATION FOR SEQ ID NO: 36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

Trp Asp Met Met Met Asn Trp Ser Pro Thr Thr Ala Leu Val Val Ser
 1           5           10           15
Gln Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala
 20           25           30
His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn
 35           40           45
Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly
 50           55           60
His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu
 65           70           75           80
Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn
 85           90           95
Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp
100          105          110
Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe
115          120          125
Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp
130          135          140
Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser
145          150          155          160
Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly
165          170          175
Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro
180          185          190
Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr
195          200          205
Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg
210          215          220
Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly
225          230          235          240
Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly
245          250          255
Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu
260          265          270
Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys

```

275	280	285
Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn 290 295 300		
Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg 305 310 315 320		
Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu 325 330 335		
Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu 340 345 350		
Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr 355 360 365		
Gly Leu Ile His Leu His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr 370 375 380		
Gly Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val 385 390 395 400		
Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu 405 410 415		
Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu 420 425 430		
Val Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser 435 440 445		
Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val 450 455 460		
Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu 465 470 475 480		
Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala 485 490		

## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1018

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide

(B) LOCATION: 2..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	
GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG	670
Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys	
210 215 220	
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC	718
Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr	

225	230	235	
TTG ACC TGC CCC ACT GAC Leu Thr Cys Pro Thr Asp 240	TGT TTT CGG AAG CAC Cys Phe Arg Lys His 245	CCC GAG GCC ACC TAC Pro Glu Ala Thr Tyr 250	766
GCC AGA TGC GGT TCT GGG Ala Arg Cys Gly Ser Gly 260	CCC TGG CTG ACA CCT Pro Trp Leu Thr Pro 265	AGG TGT ATG GTT CAT Arg Cys Met Val His 270	814
TAC CCA TAT AGG CTC TGG Tyr Pro Tyr Arg Leu Trp 275	CAC TAC CCC TGC ACT His Tyr Pro Cys Thr 280	GTC AAC TTC ACC ATC Val Asn Phe Thr Ile 285	862
TTC AAG GTT AGG ATG TAC Phe Lys Val Arg Met Tyr 290	GTG GGG GGC GTG GAG Val Gly Gly Val Glu 295	CAC AGG TTC GAA GCC His Arg Phe Glu Ala 300	910
GCA TGC AAT TGG ACT CGA Ala Cys Asn Trp Thr Arg 305	GGA GAG CGT TGT GAC Gly Glu Arg Cys Asp 310	TTG GAG GAC AGG GAT Leu Glu Asp Arg Asp 315	958
AGA TCA GAG CTT AGC CCG Arg Ser Glu Leu Ser Pro 320	CTG CTG CTG TCT ACA Leu Leu Leu Ser Thr 325	ACA GAG TGG CAG AGT Thr Thr Glu Trp Gln Ser 330	1006
GGC AGA GCT TAATTA Gly Arg Ala			1021

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val
1				5					10					15	
Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
			20					25					30		
Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val
		35				40						45			
Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe
	50					55					60				
Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser
65				70					75					80	
Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr
			85					90						95	
Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly
			100					105						110	

Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln  
 115 120 125  
 Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg  
 130 135 140  
 Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala  
 145 150 155 160  
 Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val  
 165 170 175  
 Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala  
 180 185 190  
 Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly  
 195 200 205  
 Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr  
 210 215 220  
 Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu  
 225 230 235 240  
 Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala  
 245 250 255  
 Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr  
 260 265 270  
 Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe  
 275 280 285  
 Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala  
 290 295 300  
 Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg  
 305 310 315 320  
 Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ser Gly  
 325 330 335  
 Arg Ala

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1034 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 2..1032

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..1029

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

G ATC CCA CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA	46
Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly	
1 5 10 15	
GTC CTG GCG GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG	94
Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys	
20 25 30	
GTT TTG GTT GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC	142
Val Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg	
35 40 45	
GTG TCA GGA GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC	190
Val Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu	
50 55 60	
TTT AGC CCC GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC	238
Phe Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly	
65 70 75	
AGT TGG CAC ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA	286
Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln	
80 85 90 95	
ACA GGG TTC TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT	334
Thr Gly Phe Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser	
100 105 110	
GGA TGC CCA GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT	382
Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala	
115 120 125	
CAG GGG TGG GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG	430
Gln Gly Trp Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln	
130 135 140	
AGG CCC TAC TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC	478
Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro	
145 150 155	
GCG TCT CAG GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT	526
Ala Ser Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val	
160 165 170 175	
GTG GTG GGG ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG	574
Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly	
180 185 190	
GCG AAC GAC TCG GAT GTG CTG ATT CTC AAC AAC ACG JGG CCG CCG CGA	622
Ala Asn Asp Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg	
195 200 205	

GGC AAC TGG TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys 210 215 220	670
ACG TGT GGG GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr 225 230 235	718
TTG ACC TGC CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr 240 245 250 255	766
GCC AGA TGC GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT Ala Arg Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His 260 265 270	814
TAC CCA TAT AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile 275 280 285	862
TTC AAG GTT AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala 290 295 300	910
GCA TGC AAT TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp 305 310 315	958
AGA TCA GAG CTT AGC CCG CTG CTG CTG TCT ACA ACA GGT GAT CGA GGG Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gly Asp Arg Gly 320 325 330 335	1006
CAG ACA CCA TCA CCA CCA TCA CTA AT AG Gln Thr Pro Ser Pro Pro Ser Leu 340	1034

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val 1 5 10 15
Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val 20 25 30
Leu Val Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val 35 40 45
Ser Gly Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe 50 55 60
Ser Pro Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser 65 70 75 80

(2) INFORMATION FOR SEQ ID NO: 41:

(A) LENGTH: 945 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..942

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	

AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile 195 200 205	624
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg 210 215 220	672
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu 225 230 235 240	720
ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro 245 250 255	768
TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly 260 265 270	816
GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg 275 280 285	864
TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu 290 295 300	912
TCT ACA ACA GAG TGG CAG AGC TTA ATT AAT TAG Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn 305 310	945

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala 1 5 10 15
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp 20 25 30
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile 35 40 45
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu 50 55 60
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr 65 70 75 80
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys 85 90 95

```

Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr
      100                      105                      110

Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro
      115                      120                      125

Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr
      130                      135                      140

Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly
      145                      150                      155                      160

Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu
      165                      170                      175

Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met
      180                      185                      190

Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile
      195                      200                      205

Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg
      210                      215                      220

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu
      225                      230                      235                      240

Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro
      245                      250                      255

Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly
      260                      265                      270

Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg
      275                      280                      285

Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu
      290                      295                      300

Ser Thr Thr Glu Trp Gln Ser Leu Ile Asn
      305                      310

```

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..958

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT GTG ATG CTA CTC TTT GCC	48
Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala	
1 5 10 15	
GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA GGG GCA GCA GCC TCC GAT	96
Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp	
20 25 30	
ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC GGG TCG GCT CAG AAA ATC	144
Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile	
35 40 45	
CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC ATC AAC AGG ACT GCC CTG	192
Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu	
50 55 60	
AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC TTT GCC GCA CTA TTC TAC	240
Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr	
65 70 75 80	
AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA GAG CGC TTG GCC AGC TGT	288
Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys	
85 90 95	
CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG GGT CCC CTC ACT TAC ACT	336
Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr	
100 105 110	
GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC TGC TGG CAC TAC GCG CCT	384
Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro	
115 120 125	
CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG GTG TGC GGT CCA GTG TAT	432
Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr	
130 135 140	
TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG ACG ACC GAT CGG TTT GGT	480
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly	
145 150 155 160	
GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC TCG GAT GTG CTG ATT CTC	528
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu	
165 170 175	
AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG TTC GGC TGT ACA TGG ATG	576
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met	
180 185 190	
AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG GGC CCC CCG TGC AAC ATC	624
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile	
195 200 205	
GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC CCC ACT GAC TGT TTT CGG	672
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg	
210 215 220	
AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC GGT TCT GGG CCC TGG CTG	720

Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu  
 225 230 235 240  
 ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT AGG CTC TGG CAC TAC CCC 768  
 Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro  
 245 250 255  
 TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT AGG ATG TAC GTG GGG GGC 816  
 Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly  
 260 265 270  
 GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT TGG ACT CGA GGA GAG CGT 864  
 Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg  
 275 280 285  
 TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG CTT AGC CCG CTG CTG CTG 912  
 Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu  
 290 295 300  
 TCT ACA ACA GGT GAT CGA GGG CAG ACA CCA TCA CCA CCA TCA CTA A 958  
 Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu  
 305 310 315  
 TAG 961

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe Ala  
 1 5 10 15  
 Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser Asp  
 20 25 30  
 Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys Ile  
 35 40 45  
 Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu  
 50 55 60  
 Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe Tyr  
 65 70 75 80  
 Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser Cys  
 85 90 95  
 Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr Thr  
 100 105 110  
 Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro  
 115 120 125  
 Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val Tyr

130		135		140
Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly				
145		150	155	160
Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile Leu				
	165		170	175
Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp Met				
	180		185	190
Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile				
	195		200	205
Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg				
	210		215	220
Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp Leu				
225		230	235	240
Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro				
	245		250	255
Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly				
	260		265	270
Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg				
	275		280	285
Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu				
290		295	300	
Ser Thr Thr Gly Asp Arg Gly Gln Thr Pro Ser Pro Pro Ser Leu				
305		310	315	

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1395 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1392

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1389

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG GGC CTC GCC TAC TAT

Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	
1				5					10					15		
TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	GTT	GTG	ATG	CTA	CTC	TTT	96
Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	
			20					25					30			
GCC	GGC	GTC	GAC	GGG	CAT	ACC	CGC	GTG	TCA	GGA	GGG	GCA	GCA	GCC	TCC	144
Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	
		35					40					45				
GAT	ACC	AGG	GGC	CTT	GTG	TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	192
Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	
	50					55					60					
ATC	CAG	CTC	GTA	AAC	ACC	AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	240
Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	
65					70					75					80	
CTG	AAC	TGC	AAC	GAC	TCC	CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	288
Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	
				85					90					95		
TAC	AAA	CAC	AAA	TTC	AAC	TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	336
Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	
			100					105					110			
TGT	CGC	TCC	ATC	GAC	AAG	TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	384
Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	
		115					120					125				
ACT	GAG	CCT	AAC	AGC	TCG	GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	432
Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	
	130					135						140				
CCT	CGA	CCG	TGT	GGT	ATT	GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	480
Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	
145					150					155					160	
TAT	TGC	TTC	ACC	CCG	AGC	CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	528
Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	
				165					170					175		
GGT	GTC	CCC	ACG	TAT	AAC	TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	576
Gly	Val	Pro	Thr	Tyr	Asn	Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	
			180				185						190			
CTC	AAC	AAC	ACG	CGG	CCG	CCG	CGA	GCG	AAC	TGG	TTC	GGC	TGT	ACA	TGG	624
Leu	Asn	Asn	Thr	Arg	Pro	Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	
		195					200					205				
ATG	AAT	GGC	ACT	GGG	TTC	ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	672
Met	Asn	Gly	Thr	Gly	Phe	Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	
	210					215					220					
ATC	GGG	GGG	GCC	GGC	AAC	AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	720
Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	
225					230					235					240	
CGG	AAG	CAC	CCC	GAG	GCC	ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	768
Arg	Lys	His	Pro	Glu	Ala	Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	
				245					250					255		

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CTG	ACA	CCT	AGG	TGT	ATG	GTT	CAT	TAC	CCA	TAT	AGG	CTC	TGG	CAC	TAC	816
Leu	Thr	Pro	Arg	Cys	Met	Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	
			260					265					270			
CCC	TGC	ACT	GTC	AAC	TTC	ACC	ATC	TTC	AAG	GTT	AGG	ATG	TAC	GTG	GGG	864
Pro	Cys	Thr	Val	Asn	Phe	Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	
		275					280					285				
GGC	GTG	GAG	CAC	AGG	TTC	GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	912
Gly	Val	Glu	His	Arg	Phe	Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	
	290					295					300					
CGT	TGT	GAC	TTG	GAG	GAC	AGG	GAT	AGA	TCA	GAG	CTT	AGC	CCG	CTG	CTG	960
Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	
305					310					315					320	
CTG	TCT	ACA	ACA	GAG	TGG	CAG	ATA	CTG	CCC	TGT	TCC	TTC	ACC	ACC	CTG	1008
Leu	Ser	Thr	Thr	Glu	Trp	Gln	Ile	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu	
				325					330					335		
CCG	GCC	CTA	TCC	ACC	GGC	CTG	ATC	CAC	CTC	CAT	CAG	AAC	ATC	GTG	GAC	1056
Pro	Ala	Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	
			340					345					350			
GTG	CAA	TAC	CTG	TAC	GGT	GTA	GGG	TGG	GCG	GTT	GTC	TCC	CTT	GTC	ATC	1104
Val	Gln	Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ala	Val	Val	Ser	Leu	Val	Ile	
		355					360					365				
AAA	TGG	GAG	TAT	GTC	CTG	TTG	CTC	TTC	CTT	CTC	CTG	GCA	GAC	GCG	CGC	1152
Lys	Trp	Glu	Tyr	Val	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Ala	Asp	Ala	Arg	
	370					375					380					
ATC	TGC	GCC	TGC	TTA	TGG	ATG	ATG	CTG	CTG	ATA	GCT	CAA	GCT	GAG	GCC	1200
Ile	Cys	Ala	Cys	Leu	Trp	Met	Met	Leu	Leu	Ile	Ala	Gln	Ala	Glu	Ala	
385					390					395					400	
GCC	TTA	GAG	AAC	CTG	GTG	GTC	CTC	AAT	GCG	GCG	GCC	GTG	GCC	GGG	GCG	1248
Ala	Leu	Glu	Asn	Leu	Val	Val	Leu	Asn	Ala	Ala	Ala	Val	Ala	Gly	Ala	
			405						410					415		
CAT	GGC	ACT	CTT	TCC	TTC	CTT	GTG	TTC	TTC	TGT	GCT	GCC	TGG	TAC	ATC	1296
His	Gly	Thr	Leu	Ser	Phe	Leu	Val	Phe	Phe	Cys	Ala	Ala	Trp	Tyr	Ile	
			420					425					430			
AAG	GGC	AGG	CTG	GTC	CCT	GGT	GCG	GCA	TAC	GCC	TTC	TAT	GGC	GTG	TGG	1344
Lys	Gly	Arg	Leu	Val	Pro	Gly	Ala	Ala	Tyr	Ala	Phe	Tyr	Gly	Val	Trp	
		435				440						445				
CCG	CTG	CTC	CTG	CTT	CTG	CTG	GCC	TTA	CCA	CCA	CGA	GCT	TAT	GCC	TAGTAA	1395
Pro	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Pro	Arg	Ala	Tyr	Ala		
	450					455					460					

## (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met Val Ala Gly Ala His Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr  
 1 5 10 15  
 Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Met Leu Leu Phe  
 20 25 30  
 Ala Gly Val Asp Gly His Thr Arg Val Ser Gly Gly Ala Ala Ala Ser  
 35 40 45  
 Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro Gly Ser Ala Gln Lys  
 50 55 60  
 Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His Ile Asn Arg Thr Ala  
 65 70 75 80  
 Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Phe Ala Ala Leu Phe  
 85 90 95  
 Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro Glu Arg Leu Ala Ser  
 100 105 110  
 Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp Gly Pro Leu Thr Tyr  
 115 120 125  
 Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala  
 130 135 140  
 Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln Val Cys Gly Pro Val  
 145 150 155 160  
 Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Phe  
 165 170 175  
 Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp Ser Asp Val Leu Ile  
 180 185 190  
 Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp Phe Gly Cys Thr Trp  
 195 200 205  
 Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn  
 210 215 220  
 Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys Pro Thr Asp Cys Phe  
 225 230 235 240  
 Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys Gly Ser Gly Pro Trp  
 245 250 255  
 Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr Arg Leu Trp His Tyr  
 260 265 270  
 Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val Arg Met Tyr Val Gly  
 275 280 285  
 Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu  
 290 295 300  
 Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu  
 305 310 315 320

Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys Ser Phe Thr Thr Leu  
 325 330 335  
 Pro Ala Leu Ser Thr Gly Leu Ile His Leu His Gln Asn Ile Val Asp  
 340 345 350  
 Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val Val Ser Leu Val Ile  
 355 360 365  
 Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg  
 370 375 380  
 Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile Ala Gln Ala Glu Ala  
 385 390 395 400  
 Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala Val Ala Gly Ala  
 405 410 415  
 His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile  
 420 425 430  
 Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp  
 435 440 445  
 Pro Leu Leu Leu Leu Leu Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2079

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..2076

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC GGC TTC GCC GAC CTC	48
Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp Leu	
1 5 10 15	
GTG GGG TAC ATT CCG CTC GTC GGC GCC CCC CTA GGG GGC GCT GCC AGG	96
Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala Arg	
20 25 30	

GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC GGC GTG AAC TAT GCA	144
Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala	
35 40 45	
ACA GGG AAT TTG CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG	192
Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu	
50 55 60	
CTG TCC TGT CTG ACC GTT CCA GCT FCC GCT TAT GAA GTG CGC AAC GTG	240
Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Glu Val Arg Asn Val	
65 70 75 80	
TCC GGG ATG TAC CAT GTC ACG AAC GAC TGC TCC AAC TCA AGC ATT GTG	288
Ser Gly Met Tyr His Val Thr Asn Asp Cys Ser Asn Ser Ser Ile Val	
85 90 95	
TAT GAG GCA GCG GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC	336
Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys	
100 105 110	
GTT CGG GAG AAC AAC TCT TCC CGC TGC TGG GTA GCG CTC ACC CCC ACG	384
Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu Thr Pro Thr	
115 120 125	
CTC GCA GCT AGG AAC GCC AGC GTC CCC ACC ACG ACA ATA CGA CGC CAC	432
Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr Ile Arg Arg His	
130 135 140	
GTC GAT TTG CTC GTT GGG GCG GCT GCT TTC TGT TCC GCT ATG TAC GTG	480
Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val	
145 150 155 160	
GGG GAC CTC TGC GGA TCT GTC TTC CTC GTC TCC CAG CTG TTC ACC ATC	528
Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile	
165 170 175	
TCG CCT CGC CGG CAT GAG ACG GTG CAG GAC TGC AAT TGC TCA ATC TAT	576
Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr	
180 185 190	
CCC GGC CAC ATA ACG GGT CAC CGT ATG GCT TGG GAT ATG ATG ATG AAC	624
Pro Gly His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn	
195 200 205	
TGG TCG CCT ACA ACG GCC CTG GTG GTA TCG CAG CTG CTC CGG ATC CCA	672
Trp Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro	
210 215 220	
CAA GCT GTC GTG GAC ATG GTG GCG GGG GCC CAT TGG GGA GTC CTG GCG	720
Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu Ala	
225 230 235 240	
GGC CTC GCC TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG GTT	768
Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val Leu Val	
245 250 255	
GTG ATG CTA CTC TTT GCC GGC GTC GAC GGG CAT ACC CGC GTG TCA GGA	816
Val Met Leu Leu Phe Ala Gly Val Asp Gly His Thr Arg Val Ser Gly	
260 265 270	
GGG GCA GCA GCC TCC GAT ACC AGG GGC CTT GTG TCC CTC TTT AGC CCC	864
Gly Ala Ala Ala Ser Asp Thr Arg Gly Leu Val Ser Leu Phe Ser Pro	

275	280	285	
GGG TCG GCT CAG AAA ATC CAG CTC GTA AAC ACC AAC GGC AGT TGG CAC Gly Ser Ala Gln Lys Ile Gln Leu Val Asn Thr Asn Gly Ser Trp His 290 295 300			912
ATC AAC AGG ACT GCC CTG AAC TGC AAC GAC TCC CTC CAA ACA GGG TTC Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe 305 310 315 320			960
TTT GCC GCA CTA TTC TAC AAA CAC AAA TTC AAC TCG TCT GGA TGC CCA Phe Ala Ala Leu Phe Tyr Lys His Lys Phe Asn Ser Ser Gly Cys Pro 325 330 335			1008
GAG CGC TTG GCC AGC TGT CGC TCC ATC GAC AAG TTC GCT CAG GGG TGG Glu Arg Leu Ala Ser Cys Arg Ser Ile Asp Lys Phe Ala Gln Gly Trp 340 345 350			1056
GGT CCC CTC ACT TAC ACT GAG CCT AAC AGC TCG GAC CAG AGG CCC TAC Gly Pro Leu Thr Tyr Thr Glu Pro Asn Ser Ser Asp Gln Arg Pro Tyr 355 360 365			1104
TGC TGG CAC TAC GCG CCT CGA CCG TGT GGT ATT GTA CCC GCG TCT CAG Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile Val Pro Ala Ser Gln 370 375 380			1152
GTG TGC GGT CCA GTG TAT TGC TTC ACC CCG AGC CCT GTT GTG GTG GGG Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly 385 390 395 400			1200
ACG ACC GAT CGG TTT GGT GTC CCC ACG TAT AAC TGG GGG GCG AAC GAC Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp 405 410 415			1248
TCG GAT GTG CTG ATT CTC AAC AAC ACG CGG CCG CCG CGA GGC AAC TGG Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp 420 425 430			1296
TTC GGC TGT ACA TGG ATG AAT GGC ACT GGG TTC ACC AAG ACG TGT GGG Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly 435 440 445			1344
GGC CCC CCG TGC AAC ATC GGG GGG GCC GGC AAC AAC ACC TTG ACC TGC Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys 450 455 460			1392
CCC ACT GAC TGT TTT CGG AAG CAC CCC GAG GCC ACC TAC GCC AGA TGC Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys 465 470 475 480			1440
GGT TCT GGG CCC TGG CTG ACA CCT AGG TGT ATG GTT CAT TAC CCA TAT Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr 485 490 495			1488
AGG CTC TGG CAC TAC CCC TGC ACT GTC AAC TTC ACC ATC TTC AAG GTT Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val 500 505 510			1536
AGG ATG TAC GTG GGG GGC GTG GAG CAC AGG TTC GAA GCC GCA TGC AAT Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn 515 520 525			1584
TGG ACT CGA GGA GAG CGT TGT GAC TTG GAG GAC AGG GAT AGA TCA GAG			1632

Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp	Arg	Asp	Arg	Ser	Glu		
530						535					540						
CTT	AGC	CCG	CTG	CTG	CTG	TCT	ACA	ACA	GAG	TGG	CAG	ATA	CTG	CCC	TGT	1680	
Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	Trp	Gln	Ile	Leu	Pro	Cys		
545					550					555					560		
TCC	TTC	ACC	ACC	CTG	CCG	GCC	CTA	TCC	ACC	GGC	CTG	ATC	CAC	CTC	CAT	1728	
Ser	Phe	Thr	Thr	Leu	Pro	Ala	Leu	Ser	Thr	Gly	Leu	Ile	His	Leu	His		
				565					570					575			
CAG	AAC	ATC	GTG	GAC	GTG	CAA	TAC	CTG	TAC	GGT	GTA	GGG	TCG	GCG	GTT	1776	
Gln	Asn	Ile	Val	Asp	Val	Gln	Tyr	Leu	Tyr	Gly	Val	Gly	Ser	Ala	Val		
			580					585					590				
GTC	TCC	CTT	GTC	ATC	AAA	TGG	GAG	TAT	GTC	CTG	TTG	CTC	TTC	CTT	CTC	1824	
Val	Ser	Leu	Val	Ile	Lys	Trp	Glu	Tyr	Val	Leu	Leu	Leu	Phe	Leu	Leu		
		595					600					605					
CTG	GCA	GAC	GCG	CGC	ATC	TGC	GCC	TGC	TTA	TGG	ATG	ATG	CTG	CTG	ATA	1872	
Leu	Ala	Asp	Ala	Arg	Ile	Cys	Ala	Cys	Leu	Trp	Met	Met	Leu	Leu	Ile		
	610					615					620						
GCT	CAA	GCT	GAG	GCC	GCC	TTA	GAG	AAC	CTG	GTG	GTC	CTC	AAT	GCG	GCG	1920	
Ala	Gln	Ala	Glu	Ala	Ala	Leu	Glu	Asn	Leu	Val	Val	Leu	Asn	Ala	Ala		
625					630					635					640		
GCC	GTG	GCC	GGG	GCG	CAT	GGC	ACT	CTT	TCC	TTC	CTT	GTG	TTC	TTC	TGT	1968	
Ala	Val	Ala	Gly	Ala	His	Gly	Thr	Leu	Ser	Phe	Leu	Val	Phe	Phe	Cys		
				645					650					655			
GCT	GCC	TGG	TAC	ATC	AAG	GGC	AGG	CTG	GTC	CCT	GGT	GCG	GCA	TAC	GCC	2016	
Ala	Ala	Trp	Tyr	Ile	Lys	Gly	Arg	Leu	Val	Pro	Gly	Ala	Ala	Tyr	Ala		
			660				665						670				
TTC	TAT	GGC	GTG	TGG	CCG	CTG	CTC	CTG	CTT	CTG	CTG	GCC	TTA	CCA	CCA	2064	
Phe	Tyr	Gly	Val	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Pro		
		675				680						685					
CGA	GCT	TAT	GCC	TAGTAA												2082	
Arg	Ala	Tyr	Ala														
			690														

## (2) INFORMATION FOR SEQ ID NO: 48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu		
1				5					10					15			
Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg		
		20					25						30				
Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala		

35					40					45					
Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu
	50					55					60				
Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Glu	Val	Arg	Asn	Val
	65					70					75				80
Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser	Asn	Ser	Ser	Ile	Val
				85					90					95	
Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro	Gly	Cys	Val	Pro	Cys
			100					105					110		
Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr
		115					120					125			
Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
	130						135				140				
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val
	145					150					155				160
Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile
				165					170					175	
Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr
			180					185					190		
Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn
		195					200					205			
Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
		210				215					220				
Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	Ala
	225					230					235				240
Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	Val
				245					250					255	
Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His	Thr	Arg	Val	Ser	Gly
			260					265					270		
Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val	Ser	Leu	Phe	Ser	Pro
			275				280					285			
Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	Asn	Gly	Ser	Trp	His
						295					300				
Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	Leu	Gln	Thr	Gly	Phe
	305					310					315				320
Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	Pro
				325					330					335	
Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys	Phe	Ala	Gln	Gly	Trp
			340					345					350		
Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser	Asp	Gln	Arg	Pro	Tyr
			355				360					365			
Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Ser	Gln</

370		375		380
Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser Pro Val Val Val Gly				
385		390		400
Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Asn Trp Gly Ala Asn Asp				
	405		410	415
Ser Asp Val Leu Ile Leu Asn Asn Thr Arg Pro Pro Arg Gly Asn Trp				
	420		425	430
Phe Gly Cys Thr Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly				
	435		440	445
Gly Pro Pro Cys Asn Ile Gly Gly Ala Gly Asn Asn Thr Leu Thr Cys				
	450		455	460
Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala Thr Tyr Ala Arg Cys				
	465		470	475
Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Met Val His Tyr Pro Tyr				
	485		490	495
Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile Phe Lys Val				
	500		505	510
Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Glu Ala Ala Cys Asn				
	515		520	525
Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser Glu				
	530		535	540
Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp Gln Ile Leu Pro Cys				
	545		550	555
Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu His				
	565		570	575
Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ala Val				
	580		585	590
Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu Leu Leu Phe Leu Leu				
	595		600	605
Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp Met Met Leu Leu Ile				
	610		615	620
Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Val Leu Asn Ala Ala				
	625		630	635
Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe Leu Val Phe Phe Cys				
	645		650	655
Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro Gly Ala Ala Tyr Ala				
	660		665	670
Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu Ala Leu Pro Pro				
	675		680	685
Arg Ala Tyr Ala				
690				

## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2433 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2430

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC CTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCC GAG CGG TCG CAA CCT CGT GGC AGG CGA CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCT CGC CGA CCC GAG GGT AGG GCC TGG GCT CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG GGC TGG GCA GGA TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCA CCC CGC GGC TCT CGG CCT AGT TGG GGC CCT ACA GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CGT AGG TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTT ACA TGC	384
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTC GCC GAC CTC GTG GGC TAC ATT CCG CTC GTC GGC GCC CCC CTA	432
Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu	
130 135 140	
GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG GTT CTG GAG GAC	480



Gly 145	Gly	Ala	Ala	Arg	Ala 150	Leu	Ala	His	Gly	Val 155	Arg	Val	Leu	Glu	Asp 160	
GGC Gly	GTG Val	AAC Asn	TAT Tyr	GCA Ala	ACA Thr	GGG Gly	AAT Asn	TTG Leu	CCC Pro	GGT Gly	TGC Cys	TCT Ser	TTC Phe	TCT Ser	ATC Ile	528
TTC Phe	CTC Leu	TTG Leu	GCT Ala	TTG Leu	CTG Leu	TCC Ser	TGT Cys	CTG Leu	ACC Thr	GTT Val	CCA Pro	GCT Ala	TCC Ser	GCT Ala	TAT Tyr	576
GAA Glu	GTG Val	CGC Arg	AAC Asn	GTG Val	TCC Ser	GGG Gly	ATG Met	TAC Tyr	CAT His	GTC Val	ACG Thr	AAC Asn	GAC Asp	TGC Cys	TCC Ser	624
AAC Asn	TCA Ser	AGC Ser	ATT Ile	GTG Val	TAT Tyr	GAG Glu	GCA Ala	GCG Ala	GAC Asp	ATG Met	ATC Ile	ATG Met	CAC His	ACC Thr	CCC Pro	672
GGG Gly	TGC Cys	GTG Val	CCC Pro	TGC Cys	GTT Val	CGG Arg	GAG Glu	AAC Asn	AAC Asn	TCT Ser	TCC Ser	CGC Arg	TGC Cys	TGG Trp	GTA Val	720
GCG Ala	CTC Leu	ACC Thr	CCC Pro	ACG Thr	CTC Leu	GCA Ala	GCT Ala	AGG Arg	AAC Asn	GCC Ala	AGC Ser	GTC Val	CCC Pro	ACC Thr	ACG Thr	768
ACA Thr	ATA Ile	CGA Arg	CGC Arg	CAC His	GTC Val	GAT Asp	TTG Leu	CTC Leu	GTT Val	GGG Gly	GCG Ala	GCT Ala	GCT Ala	TTC Phe	TGT Cys	816
TCC Ser	GCT Ala	ATG Met	TAC Tyr	GTG Val	GGG Gly	GAC Asp	CTC Leu	TGC Cys	GGA Gly	TCT Ser	GTC Val	TTC Phe	CTC Leu	GTC Val	TCC Ser	864
CAG Gln	CTG Leu	TTC Phe	ACC Thr	ATC Ile	TCG Ser	CCT Pro	CGC Arg	CGG Arg	CAT His	GAG Glu	ACG Thr	GTG Val	CAG Gln	GAC Asp	TGC Cys	912
AAT Asn	TGC Cys	TCA Ser	ATC Ile	TAT Tyr	CCC Pro	GGC Gly	CAC His	ATA Ile	ACG Thr	GGT Gly	CAC His	CGT Arg	ATG Met	GCT Ala	TGG Trp	960
GAT Asp	ATG Met	ATG Met	ATG Met	AAC Asn	TGG Trp	TCG Ser	CCT Pro	ACA Thr	ACG Thr	GCC Ala	CTG Leu	GTG Val	GTA Val	TCG Ser	CAG Gln	1008
CTG Leu	CTC Leu	CGG Arg	ATC Ile	CCA Pro	CAA Gln	GCT Ala	GTC Val	GTG Val	GAC Asp	ATG Met	GTG Val	GCG Ala	GGG Gly	GCC Ala	CAT His	1056
TGG Trp	GGA Gly	GTC Val	CTG Leu	GCG Ala	GGC Gly	CTC Leu	GCC Ala	TAC Tyr	TAT Tyr	TCC Ser	ATG Met	GTG Val	GGG Gly	AAC Asn	TGG Trp	1104
GCT Ala	AAG Lys	GTT Val	TTG Leu	GTT Val	GTG Val	ATG Met	CTA Leu	CTC Leu	TTT Phe	GCC Ala	GGC Gly	GTC Val	GAC Asp	GGG Gly	CAT His	1152
ACC Thr	CGC Arg	GTG Val	TCA Ser	GGA Gly	GGG Gly	GCA Ala	GCA Ala	GCC Ala	TCC Ser	GAT Asp	ACC Thr	AGG Arg	GGC Gly	CTT Leu	GTG Val	1200

TCC	CTC	TTT	AGC	CCC	GGG	TCG	GCT	CAG	AAA	ATC	CAG	CTC	GTA	AAC	ACC	1248
Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr	
				405					410					415		
AAC	GGC	AGT	TGG	CAC	ATC	AAC	AGG	ACT	GCC	CTG	AAC	TGC	AAC	GAC	TCC	1296
Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser	
			420					425					430			
CTC	CAA	ACA	GGG	TTC	TTT	GCC	GCA	CTA	TTC	TAC	AAA	CAC	AAA	TTC	AAC	1344
Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn	
			435					440					445			
TCG	TCT	GGA	TGC	CCA	GAG	CGC	TTG	GCC	AGC	TGT	CGC	TCC	ATC	GAC	AAG	1392
Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys	
		450				455					460					
TTC	GCT	CAG	GGG	TGG	GGT	CCC	CTC	ACT	TAC	ACT	GAG	CCT	AAC	AGC	TCG	1440
Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser	
			465		470					475					480	
GAC	CAG	AGG	CCC	TAC	TGC	TGG	CAC	TAC	GCG	CCT	CGA	CCG	TGT	GGT	ATT	1488
Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile	
				485					490					495		
GTA	CCC	GCG	TCT	CAG	GTG	TGC	GGT	CCA	GTG	TAT	TGC	TTC	ACC	CCG	AGC	1536
Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser	
			500					505					510			
CCT	GTT	GTG	GTG	GGG	ACG	ACC	GAT	CGG	TTT	GGT	GTC	CCC	ACG	TAT	AAC	1584
Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	Asn	
			515				520					525				
TGG	GGG	GCG	AAC	GAC	TCG	GAT	GTG	CTG	ATT	CTC	AAC	AAC	ACG	CGG	CCG	1632
Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg	Pro	
			530			535						540				
CCG	CGA	GGC	AAC	TGG	TTC	GGC	TGT	ACA	TGG	ATG	AAT	GGC	ACT	GGG	TTC	1680
Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	Phe	
					550					555					560	
ACC	AAG	ACG	TGT	GGG	GGC	CCC	CCG	TGC	AAC	ATC	GGG	GGG	GCC	GGC	AAC	1728
Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	Asn	
				565				570						575		
AAC	ACC	TTG	ACC	TGC	CCC	ACT	GAC	TGT	TTT	CGG	AAG	CAC	CCC	GAG	GCC	1776
Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys	His	Pro	Glu	Ala	
				580				585					590			
ACC	TAC	GCC	AGA	TGC	GGT	TCT	GGG	CCC	TGG	CTG	ACA	CCT	AGG	TGT	ATG	1824
Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Leu	Thr	Pro	Arg	Cys	Met	
			595				600					605				
GTT	CAT	TAC	CCA	TAT	AGG	CTC	TGG	CAC	TAC	CCC	TGC	ACT	GTC	AAC	TTC	1872
Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	Thr	Val	Asn	Phe	
			610			615					620					
ACC	ATC	TTC	AAG	GTT	AGG	ATG	TAC	GTG	GGG	GGC	GTG	GAG	CAC	AGG	TTC	1920
Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	Gly	Val	Glu	His	Arg	Phe	
					630				635						640	
GAA	GCC	GCA	TGC	AAT	TGG	ACT	CGA	GGA	GAG	CGT	TGT	GAC	TTG	GAG	GAC	1968

Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp		
				645					650					655			
AGG	GAT	AGA	TCA	GAG	CTT	AGC	CCG	CTG	CTG	CTG	TCT	ACA	ACA	GAG	TGG	2016	
Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	Trp		
			660					665						670			
CAG	ATA	CTG	CCC	TGT	TCC	TTC	ACC	ACC	CTG	CCG	GCC	CTA	TCC	ACC	GGC	2064	
Gln	Ile	Leu	Pro	Cys	Ser	Phe	Thr	Leu	Pro	Ala	Leu	Ser	Thr	Gly			
		675					680					685					
CTG	ATC	CAC	CTC	CAT	CAG	AAC	ATC	GTG	GAC	GTG	CAA	TAC	CTG	TAC	GGT	2112	
Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	Val	Gln	Tyr	Leu	Tyr	Gly		
	690					695					700						
GTA	GGG	TCG	GCG	GTT	GTC	TCC	CTT	GTC	ATC	AAA	TGG	GAG	TAT	GTC	CTG	2160	
Val	Gly	Ser	Ala	Val	Val	Ser	Leu	Val	Ile	Lys	Trp	Glu	Tyr	Val	Leu		
705					710					715					720		
TTG	CTC	TTC	CTT	CTC	CTG	GCA	GAC	GCG	CGC	ATC	TGC	GCC	TGC	TTA	TGG	2208	
Leu	Leu	Phe	Leu	Leu	Leu	Ala	Asp	Ala	Arg	Ile	Cys	Ala	Cys	Leu	Trp		
				725					730					735			
ATG	ATG	CTG	CTG	ATA	GCT	CAA	GCT	GAG	GCC	GCC	TTA	GAG	AAC	CTG	GTG	2256	
Met	Met	Leu	Leu	Ile	Ala	Gln	Ala	Glu	Ala	Ala	Leu	Glu	Asn	Leu	Val		
		740						745					750				
GTC	CTC	AAT	GCG	GCG	GCC	GTG	GCC	GGG	GCG	CAT	GGC	ACT	CTT	TCC	TTC	2304	
Val	Leu	Asn	Ala	Ala	Ala	Val	Ala	Gly	Ala	His	Gly	Thr	Leu	Ser	Phe		
		755					760					765					
CTT	GTG	TTC	TTC	TGT	GCT	GCC	TGG	TAC	ATC	AAG	GGC	AGG	CTG	GTC	CCT	2352	
Leu	Val	Phe	Phe	Cys	Ala	Ala	Trp	Tyr	Ile	Lys	Gly	Arg	Leu	Val	Pro		
	770					775					780						
GGT	GCG	GCA	TAC	GCC	TTC	TAT	GGC	GTG	TGG	CCG	CTG	CTC	CTG	CTT	CTG	2400	
Gly	Ala	Ala	Tyr	Ala	Phe	Tyr	Gly	Val	Trp	Pro	Leu	Leu	Leu	Leu	Leu		
785				790					795						800		
CTG	GCC	TTA	CCA	CCA	CGA	GCT	TAT	GCC	TAGTAA							2433	
Leu	Ala	Leu	Pro	Pro	Arg	Ala	Tyr	Ala									
				805				810									

## (2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 809 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn		
1				5					10					15			
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly		
			20					25					30				
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala		

35					40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
	50					55					60				
Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly
65					70					75					80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
		115					120				125				
Gly	Phe	Ala	Asp	Leu	Val	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu
	130					135					140				
Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp
145					150					155					160
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile
				165					170					175	
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr
			180					185					190		
Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	Cys	Ser
		195					200					205			
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	His	Thr	Pro
	210					215					220				
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Val
225					230					235					240
Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr
				245					250					255	
Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys
			260					265					270		
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Ser
		275					280					285			
Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	Arg	His	Glu	Thr	Val	Gln	Asp	Cys
	290					295					300				
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp
305					310					315					320
Asp	Met	Met	Met	Asn	Trp	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln
				325					330					335	
Leu	Leu	Arg	Ile	Pro	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His
			340					345					350		
Trp	Gly	Val	Leu	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp
		355					360					365			
Ala	Lys	Val	Leu	Val	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly	His

370					375					380					
Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Ala	Ser	Asp	Thr	Arg	Gly	Leu	Val
385					390					395					400
Ser	Leu	Phe	Ser	Pro	Gly	Ser	Ala	Gln	Lys	Ile	Gln	Leu	Val	Asn	Thr
				405					410					415	
Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	Thr	Ala	Leu	Asn	Cys	Asn	Asp	Ser
			420					425					430		
Leu	Gln	Thr	Gly	Phe	Phe	Ala	Ala	Leu	Phe	Tyr	Lys	His	Lys	Phe	Asn
		435					440					445			
Ser	Ser	Gly	Cys	Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Ser	Ile	Asp	Lys
	450					455					460				
Phe	Ala	Gln	Gly	Trp	Gly	Pro	Leu	Thr	Tyr	Thr	Glu	Pro	Asn	Ser	Ser
465					470					475					480
Asp	Gln	Arg	Pro	Tyr	Cys	Trp	His	Tyr	Ala	Pro	Arg	Pro	Cys	Gly	Ile
				485					490					495	
Val	Pro	Ala	Ser	Gln	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser
			500					505					510		
Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Phe	Gly	Val	Pro	Thr	Tyr	Asn
		515					520					525			
Trp	Gly	Ala	Asn	Asp	Ser	Asp	Val	Leu	Ile	Leu	Asn	Asn	Thr	Arg	Pro
	530					535					540				
Pro	Arg	Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Gly	Thr	Gly	Phe
545					550					555					560
Thr	Lys	Thr	Cys	Gly	Gly	Pro	Pro	Cys	Asn	Ile	Gly	Gly	Ala	Gly	Asn
				565					570					575	
Asn	Thr	Leu	Thr	Cys	Pro	Thr	Asp	Cys	Phe	Arg	Lys	His	Pro	Glu	Ala
			580					585					590		
Thr	Tyr	Ala	Arg	Cys	Gly	Ser	Gly	Pro	Trp	Leu	Thr	Pro	Arg	Cys	Met
		595					600					605			
Val	His	Tyr	Pro	Tyr	Arg	Leu	Trp	His	Tyr	Pro	Cys	Thr	Val	Asn	Phe
	610					615					620				
Thr	Ile	Phe	Lys	Val	Arg	Met	Tyr	Val	Gly	Gly	Val	Glu	His	Arg	Phe
625					630					635					640
Glu	Ala	Ala	Cys	Asn	Trp	Thr	Arg	Gly	Glu	Arg	Cys	Asp	Leu	Glu	Asp
				645					650				655		
Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Ser	Thr	Thr	Glu	Trp
			660					665					670		
Gln	Ile	Leu	Pro	Cys	Ser	Phe	Thr	Thr	Leu	Pro	Ala	Leu	Ser	Thr	Gly
		675					680					685			
Leu	Ile	His	Leu	His	Gln	Asn	Ile	Val	Asp	Val	Gln	Tyr	Leu	Tyr	Gly
	690					695					700				

Val Gly Ser Ala Val Val Ser Leu Val Ile Lys Trp Glu Tyr Val Leu  
 705 710 715 720  
 Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile Cys Ala Cys Leu Trp  
 725 730 735  
 Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val  
 740 745 750  
 Val Leu Asn Ala Ala Ala Val Ala Gly Ala His Gly Thr Leu Ser Phe  
 755 760 765  
 Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro  
 770 775 780  
 Gly Ala Ala Tyr Ala Phe Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu  
 785 790 795 800  
 Leu Ala Leu Pro Pro Arg Ala Tyr Ala  
 805

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Ser Asn Ser Ser Glu Ala Ala Asp Met Ile Met His Thr Pro Gly Cys  
 1 5 10 15  
 Val

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1..22

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Gly Gly Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
 1 5 10 15  
 Ser Pro Thr Thr Ala Leu  
 20

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..37

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1 5 10 15  
 Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 20 25 30  
 Pro Gly Cys Gly Lys  
 35

## (2) INFORMATION FOR SEQ ID NO: 54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gly Gly Thr Pro Thr Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr  
 1 5 10 15  
 Gln Leu Arg Arg His Ile Asp Leu Leu  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

Gly Gly Thr Pro Thr Leu Ala Ala Arg Asp Ala Ser Val Pro Thr Thr
1           5           10           15
Thr Ile Arg Arg His Val Asp Leu Leu
          20           25

```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
1           5           10           15
Ser Thr Gly Leu
          20

```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp Cys Pro
1           5           10           15
Asn Ser Ser Ile
          20

```



## (2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala His Asp Ala Ile  
 1                      5                      10                      15  
 Leu His Thr Pro  
                     20

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr  
 1                      5                      10                      15  
 Pro Gly Cys Val  
                     20

## (2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

His Asp Ala Ile Leu His Thr Pro Gly Val Pro Cys Val Arg Glu Gly  
 1                      5                      10                      15  
 Asn Val Ser

## (2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Cys	Val	Arg	Glu	Gly	Asn	Val	Ser	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro
1				5					10					15	
Thr	Val	Ala	Thr												
			20												

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	Lys	Leu	Pro	Ala	Thr
1				5					10					15	
Gln	Leu	Arg	Arg												
			20												

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	Gly	Ser
1				5					10					15	
Ala	Thr	Leu	Cys												
			20												

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu
1           5           10          15
Cys Gly Ser Val
                20

```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr Thr Gln Gly Cys
1           5           10          15
Asn Cys Ser Ile
                20

```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
1           5           10          15
Arg Met Ala Trp
                20

```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro
1              5              10              15
Thr Ala Ala Leu
                20

```

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

Asn Trp Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile
1              5              10              15
Pro Gln Ala Ile
                20

```

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

Leu Leu Arg Ile Pro Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His
1              5              10              15
Trp Gly Val Leu
                20

```

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met  
 1 5 10 15  
 Val Gly Asn Met  
 20

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala Glu Thr Ile Val Ser  
 1 5 10 15  
 Gly Gly Gln Ala  
 20

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln Asn Ile Gln  
 1 5 10 15  
 Leu Ile Asn Thr  
 20

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Gln Asn Ile Gln Leu Ile Asn Thr Asn Gly Gln Trp His Ile Asn Ser  
 1 5 10 15  
 Thr Ala Leu Asn  
 20

## (2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Leu Asn Cys Asn Glu Ser Leu Asn Thr Gly Trp Trp Leu Ala Gly Leu  
 1 5 10 15  
 Ile Tyr Gln His Lys  
 20

## (2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Gly Leu Ile Tyr Gln His Lys Phe Asn Ser Ser Gly Cys Pro Glu  
 1 5 10 15  
 Arg Leu Ala Ser  
 20

## (2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Gly Cys Pro Glu Arg Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp

1                      5                      10                      15  
 Gln Gly Trp Gly  
 20

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asp Phe Asp Gln Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser  
 1                      5                      10                      15  
 Gly Pro Asp Gln  
 20

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Asn Gly Ser Gly Pro Asp Gln Arg Pro Tyr Cys Trp His Tyr Pro  
 1                      5                      10                      15  
 Pro Lys Pro Cys  
 20

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Trp His Tyr Pro Pro Lys Pro Cys Gly Ile Val Pro Ala Lys Ser Val  
 1                      5                      10                      15  
 Cys Gly Pro Val

20

## (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala	Lys	Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val
1				5				10					15		
Val Val Gly Thr															
20															

## (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Pro	Ser	Pro	Val	Val	Val	Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala	Pro	Thr
1				5				10					15		
Tyr Ser Trp Gly															
20															

## (2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gly	Ala	Pro	Thr	Tyr	Ser	Trp	Gly	Glu	Asn	Asp	Thr	Asp	Val	Phe	Val
1				5				10					15		
Leu Asn Asn Thr															
20															

## (2) INFORMATION FOR SEQ ID NO: 83:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Gly	Asn	Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Ser	Thr	Gly	Phe	Thr	Lys
1				5				10						15	
Val	Cys	Gly	Ala												
			20												

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Gly	Phe	Thr	Lys	Val	Cys	Gly	Ala	Pro	Pro	Val	Cys	Ile	Gly	Gly	Ala
1				5				10						15	
Gly	Asn	Asn	Thr												
			20												

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ile	Gly	Gly	Ala	Gly	Asn	Asn	Thr	Leu	His	Cys	Pro	Thr	Asp	Cys	Arg
1				5				10						15	
Lys	His	Pro													

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Ser Arg Cys Gly  
 1                      5                      10                      15  
 Ser Gly Pro Trp  
 20

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Ser Arg Cys Gly Ser Gly Pro Trp Ile Thr Pro Arg Cys Leu Val Asp  
 1                      5                      10                      15  
 Tyr Pro Tyr Arg  
 20

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Cys Leu Val Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile  
 1                      5                      10                      15  
 Asn Tyr Thr Ile  
 20

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly  
1 5 10 15

Gly Val Glu His  
20

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys Asn Trp  
1 5 10 15

Thr Pro Gly Glu  
20

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Ala Cys Asn Trp Thr Pro Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp  
1 5 10 15

Arg Ser Glu Leu  
20

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Glu	Asp	Arg	Asp	Arg	Ser	Glu	Leu	Ser	Pro	Leu	Leu	Leu	Thr	Thr	Thr
1				5				10					15		
Gln Trp Gln Val															
20															

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu
1				5				

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

ACGTCCGTAC GTTCGAATTA ATTAATCGA

29

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CCTCCGGACG TGCCTAGCT CCCGTCTGIG GTAGTGGTGG TAGTGATTAT CAATTAATTG

60

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GTTTAACCAC TGCATGATG

19

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

GTCCCATCGA GTGCGGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTGACATGG TACATTCCGG ACACTTGGCG CACTTCATAA GCGGA

45

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TGCCTCATAC ACAATGGAGC TCTGGGACGA GTCGTTCTGTG AC

42

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TACCCAGCAG CGGGAGCTCT GTTGCTCCCG AACGCAGGGC AC

42

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TGTCGTGGTG GGGACGGAGG CCTGCCTAGC TGCGAGCGTG GG

42

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGTTATGTGG CCCGGGTAGA TTGAGCACTG GCAGTCCTGC ACCGTCTC

48

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CAGGGCCGTT CTAGGCCTCC ACTGCATCAT CATATCCCAA GC

42

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CCGGAATGTA CCATGTCACG AACGAC

26

## (2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
GCTCCATTGT GTATGAGGCA GCGG

24

## (2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:  
GAGCTCCCGC TGCTGGGTAG CGC

23

## (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:  
CCTCCGTCCC CACCACGACA ATACG

25

## (2) INFORMATION FOR SEQ ID NO: 108:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CTACCCGGGC CACATAACGG GTCACCG

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGAGGCCTAC AACGGCCCTG GTGG

24

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TTCTATCGAT TAAATAGAAT TC

22

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid

23

## (2) INFORMATION FOR SEQ ID NO: 112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys  
 1                      5                      10                      15  
 Ser Asn Ser Ser  
                     20

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp  
 1                      5                      10                      15  
 Met Ile Met His Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Ala Ala Asp Met Ile Met His Thr Pro Gly Cys Val Pro Cys Val  
 1                      5                      10                      15

Arg Glu Asn Asn Ser  
20

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val Ala Leu  
1                      5                      10                      15

Thr Pro Thr Leu Ala  
20

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro  
1                      5                      10                      15

Thr Thr Thr Ile Arg  
20

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 1             5             10             15

Gly Ala Ala Ala Phe
                20

```

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly
 1             5             10             15

Asp Leu Cys Gly Ser
                20

```

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ser Gln Leu
 1             5             10             15

Phe Thr Ile Ser Pro
                20

```

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

Ser Gln Leu Phe Thr Ile Ser Pro Arg Arg His Glu Thr Val Gln  
1 5 10 15

Asp Cys Asn Cys Ser  
20

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr  
1 5 10 15

Gly His Arg Met Ala  
20

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp  
1 5 10 15  
Ser Pro Thr Thr Ala  
20